

1 ATGAACAAGTTGCTGTGCTGCGCGCTCGTGTTCCTGGACAT
M N K L L C C A L V F L D I
42 CTCCATTAAAGTGGACCACCCAGGAAACGTTTCCTCCAAAGT
S I K W T T Q E T F P P K
83 ACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGT
Y L H Y D E E T S H Q L L C
124 GACAAATGTCCTCTCTGGTACCTACCTAAAACAACACTGTAC
D K C P P G T Y L K Q H C T
165 AGCAAAGTGGAAGACCGTGTGCGCCCCCTTGCCCTGACCACT
A K W K T V C A P C P D H
206 ACTACACAGACAGCTGGCACACCAGTGACGAGTGTCTATAC
Y Y T D S W H T S D E C L Y
247 TGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGA
C S P V C K E L Q Y V K Q E
288 GTGCAATCGCACCCACAACCGCGTGTGCGAATGCAAGGAAG
C N R T H N R V C E C K E
329 GCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGC
G R Y L E I E F C L K H R S
370 TGCCCTCCTGGATTTGGAGTGGTGAAGCTGGAACCCCAGA
C P P G F G V V Q A G T P E
411 GCGAAATACAGTTTGCAAAAGATGTCCAGATGGGTTCCTCT
R N T V C K R C P D G F F
452 CAAATGAGACGTCATCTAAAGCACCCCTGTAGAAAACACACA
S N E T S S K A P C R K H T
493 AATTGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAA
N C S V F G L L L T Q K G N
534 TGCAACACACGACAACATATGTTCCGGAAACAGTGAATCAA
A T T V D N T C C C N C F C

2 / 5 MATCH WITH FIG. 1A

575 CTCAAAAATGTGGAATAGATGTTACCCCTGTGTGAGGAGGCA
T Q K C G I D V T L C E E A
616 TTCTTCAGGTTTGCTGTTCCTACAAAGTTTACGCCTAACTG
F F R F A V P T K F T P N W
657 GCTTAGTGTCTTGGTAGACAATTTCCTGGCACCAAAGTAA
L S V L V D N L P G T K V
698 ACGCAGAGAGTGTAGAGAGGATAAAACGGCAACACAGCTCA
N A E S V E R I K R Q H S S
739 CAAGAACAGACTTTCAGCTGCTGAAGTTATGGAAACATCA
Q E Q T F Q L L K L W K H Q
780 AAACAAAGACCAAGATATAGTCAAGAAGATCATCCAAGATA
N K D Q D I V K K I I Q D
821 TTGACCTCTGTGAAAACAGCGTGCAGCGGCACATTGGACAT
I D L C E N S V Q R H I G H
862 GCTAACCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAAAG
A N L T F E Q L R S L M E S
903 CTTACCGGGAAAGAAAGTGGGAGCAGAAGACATTGAAAAAA
L P G K K V G A E D I E K
944 CAATAAAGGCATGCAAACCCAGTGACCAGATCCTGAAGCTG
T I K A C K P S D Q I L K L
985 CTCAGTTTGTGGCGAATAAAAAATGGCGACCAAGACACCTT
L S L W R I K N G D Q D T L
1026 GAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACC
K G L M H A L K H S K T Y
1067 ACTTTCCACAAACTGTCACTCAGAGICTAAAGAAGACCAT
H F P T N C H S E S K E D H
1108 CAGGTTCCCTTCACAGCTTCACAATGTACAAATTGTATCAGA
Q V P S Q L H N V Q I V S E
1149 AGTTATTTTTAGAAATGATAGGTAA

FIG. 2A

tnfr2.msf{TNFR2_LIKE}	1MNKLL	CCALVFLDIS	IKWTTQETFP	P.....	KYLHYDEETS	50
tnfr2.msf{TNR2_HUMAN}		MAPVAVWAAL	AVGLELWAAA	HALPAQVAFT	PYAPEPGSTC	RLREYDQTA	
Consensus		-----L	---L-----	-----Q--F-	P-----	-----Y---T-	
tnfr2.msf{TNFR2_LIKE}	51	HQLLCDKCPP	GTYLKQHCTA	KWKTVCAPCP	DHYTDSWHT	SDECLYCSVP	100
tnfr2.msf{TNR2_HUMAN}		.QMCCSKCSP	GQHAKVFTK	TSDTVCDSC	DSTYTQLWNW	VPECLSCGSR	
Consensus		-Q--C-KC-P	G---K--CT-	---TVC--C-	D--YT--W--	--ECL-C---	
tnfr2.msf{TNFR2_LIKE}	101	CKELQYVKQE	CNRTNVRCE	CKEGRYLEIEFCLK	HRSCPPGFGV	150
tnfr2.msf{TNR2_HUMAN}		CSSDQVETQA	CTREQNRIC	CRPGWYCAL	KQEGCRLCAP	LRKCRPGFGV	
Consensus		C---Q---Q-	C-R--NR-C-	C--G-Y----	-----C--	-R-C-PGFGV	
tnfr2.msf{TNFR2_LIKE}	151	VQAGTPERN	VCKRCPDGF	SNETSSKAPC	RKHTNCSVFG	LLLTQKGNAT	200
tnfr2.msf{TNR2_HUMAN}		ARPGTETSD	VCKPCAPGT	SNNTSSTDIC	RPHQICNVVA	I....PGNAS	
Consensus		---GT-----	VCK-C--G-F	SN-TSS---C	R-H--C-V--	-----GNA-	
tnfr2.msf{TNFR2_LIKE}	201	HDNIC.....SGNSE	STQKCGIDVT	LCEEAFF...	250
tnfr2.msf{TNR2_HUMAN}		RDAVCTSTSP	TRSMAPGAVH	LPQPVSTRSQ	HTQPTPEPST	APSTSFLPM	
Consensus		-D--C-----	-----	-----S--S-	-TQ-----T	-----F----	

MATCH WITH FIG. 2B

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FIG. 2B

MATCH WITH FIG. 2A

251
 ifr2.msf(TNFR2_LIKE)
 ifr2.msf(TNFR2_HUMAN)
 Consensus

301
 ifr2.msf(TNFR2_LIKE)
 ifr2.msf(TNFR2_HUMAN)
 Consensus

351
 ifr2.msf(TNFR2_LIKE)
 ifr2.msf(TNFR2_HUMAN)
 Consensus

401
 ifr2.msf(TNFR2_LIKE)
 ifr2.msf(TNFR2_HUMAN)
 Consensus

451
 ifr2.msf(TNFR2_LIKE)
 ifr2.msf(TNFR2_HUMAN)
 Consensus

MATCH WITH FIG. 2C

251
 RFAVPTKFT PNWLSVLVDN LPGTKVNAES VERIKR....
 GPSPPAEGST GDFALPVGLI VG..VTALGL LIIGVVNCVI MTQVKKKPLC
 ----- -FA-P----- L-----VN-----K-----

301
 .QHSSQEQTFF QLLKLWKHQN KDQDIV.... .KKIIQDIDL CENSVQRHIG
 LQREAKVPHL PADKARGTQG PEQQHLLITA PSSSSSSLES SASALDRRAP
 -Q----- -K---Q- --Q-----R-----

351
 HANLTFEQLR SLMESLPGKK VGEAEDIEKTI KACKPSDQIL KLLSLWRIKN
 TRNOP..QAP GVEASGAGEA RASTGSSDSS PGHGTQ..V NVTCTVNVCS
 --N---Q-- ---S-G-- --- --- ---

401
 GDQDTLKGLM HALKHSKTYH FPTNCHSESK EDHQVPSQLH NVOIVSEVIF
 SSDHSSQCSS QA...SSTMG DTDSSPSESP KDEQVPFSKE ECAFRSQLET
 ----- -A---S-T-- -----SES--D-QVP-----S-----

451
 RNDR.....
 PETLLGSTEE KPLPLGVPDA GMKPS

MATCH WITH FIG. 2B

FIG. 2C

Query: 38 QLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSPVCKELQYVKQEC 97
 Q+ C KC PG + K CT TVC C D YT W+ ECL C C Q Q C

Sbjct: 29 QMCCSKCSPGQHAKVFC TKTS DTVCDSCEDSTYTQLWNWVPECLSCGSRCSDDQVETQAC 88

Query: 98 NRTHNRVCECKEGRYLEIEFCLKHRSCPP 126

R NR+C C+ G Y + R C P

Sbjct: 89 TREQNRICRPGWYCALSKQEGCRLCAP 117

Query: 118 CLKHRSCPPGFGVVQAGTPERNVCKRCPDGFNETSSKAPCRKHTNCSVFGL 171

C R C PGFGV + GT + VCK C G FSN TSS CR H C+V +

Sbjct: 115 CAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSTTSSTDICRPHQICNVVAI 168

Query: 177 GNATHDNICSGNS 189

GNA+ D +C+ S

Sbjct: 170 GNASMDAVCTSTS 182

Query: 363 SESKEDHQVP 372

SES +D QVP

Sbjct: 391 SESPKDEQVP 400